



Sequence Revision History

PubMed

Nucleotide

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Genome

Structure

PMC

Taxonomy

OMIM

Books

Find (Accession, GI number or Fasta style SeqId)





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Revision history for "AF027217"			
GI	Version	Update Date	Status
2689645	1	Sep 24 1998 17:14	Live
2689645	1	May 14 1998 13:09	Dead
2689645	1	Dec 17 1997 0:15	Dead

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Accession <u>AF027217</u> was first seen at <u>NCBI</u> on Dec 17 1997 0:15

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LinkOut

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Reference sequence project

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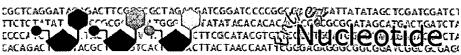
Revised: July 5, 2002.

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Mar 17 2003 10:55:57





PubMed Nucleotide Protein **PMC** Genome Structure Taxonomy OMIM Boo Search Nucleotide for Limits Preview/Index History Clipboard Details Get Subsequence default Show: 20 File Send to Display

☐ 1: AF027217. Porcine circoviru...[gi:2689645]

Links

LOCUS AF027217 1768 bp DNA circular VRL 14-MAY-1998

DEFINITION Porcine circovirus strain pmws PCV, complete genome.

ACCESSION AF027217

VERSION AF027217.1 GI:2689645

KEYWORDS

SOURCE Porcine circovirus
ORGANISM Porcine circovirus

Viruses; ssDNA viruses; Circoviridae; Circovirus.

REFERENCE 1 (bases 1 to 1768)

AUTHORS Hamel, A.L., Lin, L.L. and Nayar, G.P.

TITLE Nucleotide sequence of porcine circovirus associated with

postweaning multisystemic wasting syndrome in pigs

JOURNAL J. Virol. 72 (6), 5262-5267 (1998)

MEDLINE <u>98241772</u> PUBMED <u>9573301</u>

REFERENCE 2 (bases 1 to 1768)

AUTHORS Hamel, A.L., Lin, L.L. and Nayar, G.P.S.

TITLE Direct Submission

JOURNAL Submitted (26-SEP-1997) Virology Laboratory, Veterinary Services

Branch, Manitoba Agriculture, 545 University Crescent, Winnipeg,

Manitoba R3T 5S6, Canada

FEATURES Location/Qualifiers

source 1..1768

/organism="Porcine circovirus"

/strain="pmws PCV"
/db_xref="taxon:46221"

/note="both strands of seven overlapping PCR fragments were sequenced; virus isolated from lung, lymph node, spleen and tonsil tissue from pigs affected by post

weaning multisystemic wasting syndrome"

<u>CDS</u> complement(join(1732..1768,1..92))

/note="ORF9; predicted 4.6 kDa protein"

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/translation="MWLGSASSILLAGHVAAEVLPRCCRCRSALVILTAHFFRFQL"

stem loop join(1746..1768,1..13)

/function="putative replication site"

<u>rep_origin</u> join(1762..1768,1..2)

/note="'AAGTATTAC' is similar to the nonanucleotide motif

in the non-pathogenic PCV, GenBank Accession Number

U49186"

CDS 51..995

/note="ORF1; similar to Rep protein encoded by

non-pathogenic PCV, GenBank Accession Number U49186;

predicted 35.8 kDa protein"

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misc feature
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                /translation="MDIDHTVSVDHPTAASHKSHO"
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                     FTPKPVLDSTIDYFQPNNKRTQLWLRLQTSRNVDHVGLGTAFENSIYDODYNIRVTMY
                     VOFREFNLKDPPLKP"
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                                  495 g
                                           461 t
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       61 agaagaatgg aagaagcgga ccccaaccac ataaaaggtg ggtgttcacg ctgaataatc
      121 cttccgaaga cgagcgcaag aaaatacggg agctcccaat ctccctattt gattatttta
      181 ttgttggcga ggagggtaat gaggaaggac gaacacctca cctccagggg ttcgctaatt
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